

# Clarity

## *Clarity cooperation with LIMS systems*

ENG

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To facilitate the orientation in the **Clarity cooperation with LIMS systems** manual and **Clarity** chromatography station, different fonts are used throughout the manual. Meanings of these fonts are:

**Instrument** (blue text) marks the name of the window, to which the text refers.

*Open File* (italics) describes the commands and names of fields in **Clarity**, parameters that can be entered into them or a window or dialog name (when you already are in the topic describing the window).

WORK1 (capitals) indicates the name of the file and/or directory.

*ACTIVE* (capital italics) marks the state of the station or its part.

The bold text is sometimes also used for important parts of the text and the name of the **Clarity** station. Moreover, there are text sections written in format other than normal text. These sections are formatted as follows:

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**Note:** Notifies the reader of possibly interesting information.

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**Caution:** Warns the user of possibly dangerous or very important information.

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**█ Marks the problem statement or trouble question.**

**Description:** Presents any closer information on the problem, describes its causes etc.

**Solution:** Marks the response to the question, presents a procedure how to remove it.

# 1 Clarity cooperation with LIMS systems

**Clarity** can be connected to any **LIMS** using the **import/export** of **text files**. The results can be exported in various formats to the **LIMS** and the sample info can be imported from a text file to **Clarity** sequence to be processed.

There is a dedicated program interface **LimsLink** which can be used as an intermediate, see

<http://www.dataapex.com/product.php?id=limslink.php>.

However most **LIMS** systems will be able to handle the import/export of the text data directly.

The tasks usually comprise from import of sample data information generated by **LIMS** to **Clarity** sequence table and exporting the results from **Clarity** in a format suitable for import to the **LIMS**.

## 2 Import data to Sequence

Common approach is to copy the range of selected cells from a spreadsheet and paste it to the sequence table as you are used to do so in Excel.

But we recommend to use the import functions provided in **Clarity** which can automate the data import from **LIMS** to **Clarity**.

To create a sequence table from a text file, the suggested procedure will be using the *File - Import* command in the **Sequence** window ①.

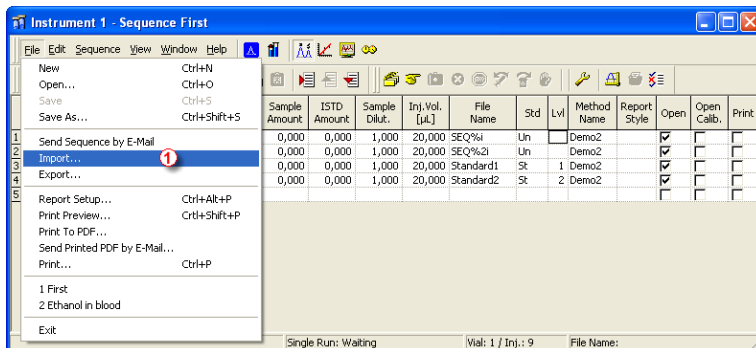


Fig 1: Importing Sequence

In **Step 1** you will select the file to import (will be remembered).

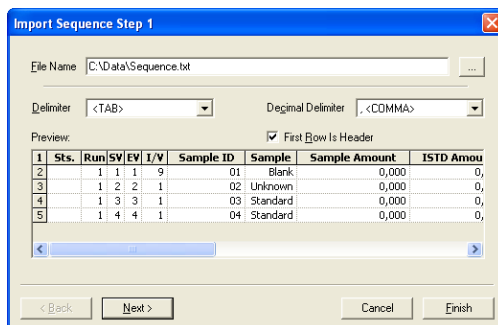


Fig 2: First step of importing Sequence

In the **Step 2** you will map the text file columns to the *Sequence* table columns – in case the same column headers will be used, it will be set automatically for most of them, the settings can be remembered (check box *Save Import Settings*). The imported file must contain at least the *File Name*, other fields will be replaced by defaults values (new sequence) or from preceding line (append to existing sequence).

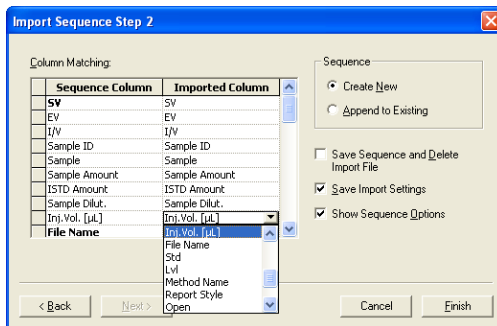


Fig 3: Second step of importing sequence

If you check *Show Sequence Options*, the respective window will be shown.

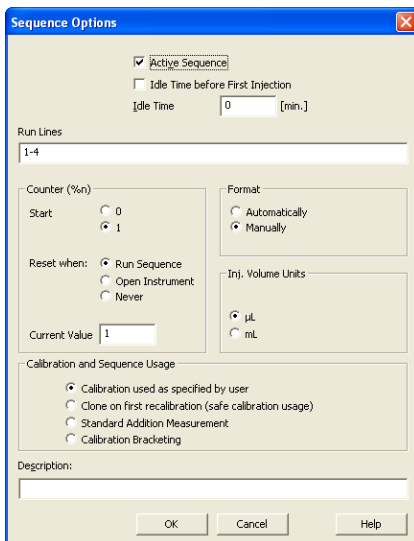


Fig 4: Sequence Options dialog

Note also the TEMPLATE.SEQ in the COMMON folder (located in C:\CLARITY by default) – this file is used to create a new sequence and can be amended to contain besides the desired sequence options also repeatedly used calibration standard and control samples lines – just to add the unknowns.

To automate the operation you can use the command line parameter: *seq\_import\_append*

- This parameter imports specified file and adds it to the opened sequence using the current settings for manual sequence import; functional from

**Clarity** version **2.8.3**).

- Supported file type is \*.TXT.
- Syntax: *seq\_import\_append=c:\tmp\seq.txt*
- Possible values: valid path.
- Implicit value: none.

When using the **Single Run** dialog in **Clarity**, it is possible to use command line parameter, which preset the *Sample* name in the **Single Run** dialog. Remember to add the %Q variable to the *Chromatogram File Name*, then the measured chromatogram will contain the *Sample* in their names. The syntax is:

*set\_sample\_name*

- Sets sample name parameter for the next single run. It is possible to set the Instrument by the i=(number of Instrument) parameter.
- Syntax: *set\_sample\_name=text*
- Possible values: Any non-empty text.
- Implicit value: None.

## 3 Export Results Data

There may be two approaches to transfer the results to **LIMS** – either your method is robust enough, that you can do so automatically after the run is finished or (more commonly) you will want to export the results after reviewing and amending them in **Clarity**.

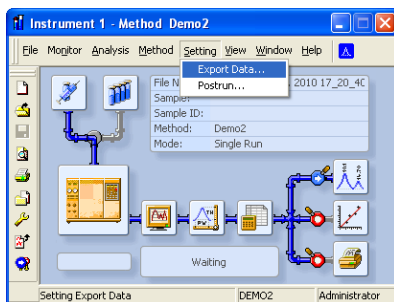


Fig 5: Export Data menu in the Instrument window

For export data you can set the desired format in the **Export Data** dialog using the **Settings - Export Data...** menu in the **Instrument** window.

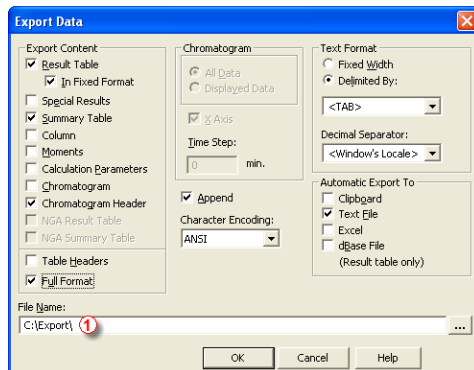


Fig 6: Export Data dialog

Please check the **Reference Guide** or **Help** for a detailed description of the available options – some experimenting to get the most suitable combination to obtain the exported data in a convenient format may be necessary. Note entire summary table can be exported for all the opened chromatograms. In the *File Name* field enter the export path without the file name ①. The file name will be generated from the chromatogram file name and the appropriate suffix will be added.

The export of data can be performed in various ways:

- Automatically after each single run according to the settings in **PostRun Setting** dialog accessible from the **Instrument** window via the menu *Setting - Postun...*:

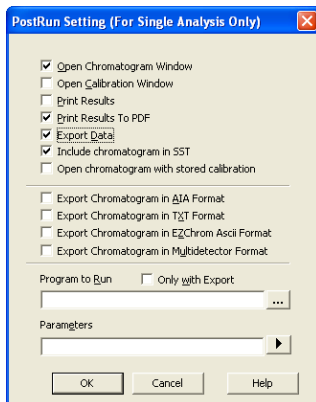


Fig 7: PostRun Setting dialog

- Separately for each line in sequence (the respective columns are hidden by default):

Sts.	Run	SV	EV	I/V	Sample ID	Sample	Sample Amount	ISTD Amount	Sample Dilut.	Inj. Vol. [µL]	File Name	Std	Lvl	Method Name	Report Style	Open	Open Calib.	Print	Export Data
1	✓	1	1	9	01	Blank	0,000	0,000	1,000	20,000	SEQ%4	Un		Demo2		✓	✓	✓	✓
2	✓	2	2	1	02	Unknown	0,000	0,000	1,000	20,000	SEQ%2i	Un		Demo2		✓	✓	✓	✓
3	✓	3	3	1	03	Standard1	0,000	0,000	1,000	20,000	Standard1	St	1	Demo2		✓	✓	✓	✓
4	✓	4	4	1	04	Standard2	0,000	0,000	1,000	20,000	Standard2	St	2	Demo2		✓	✓	✓	✓
5																			

Fig 8: Export option in column of the Sequence table

- Or using the **Batch** in selected chromatograms eventually entire sequence after they have been reviewed:

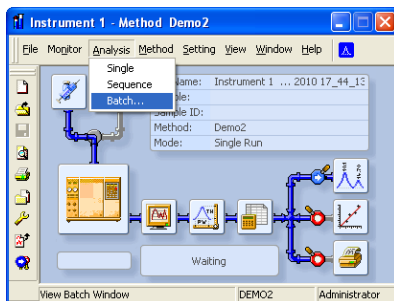


Fig 9: Batch menu in the Instrument window

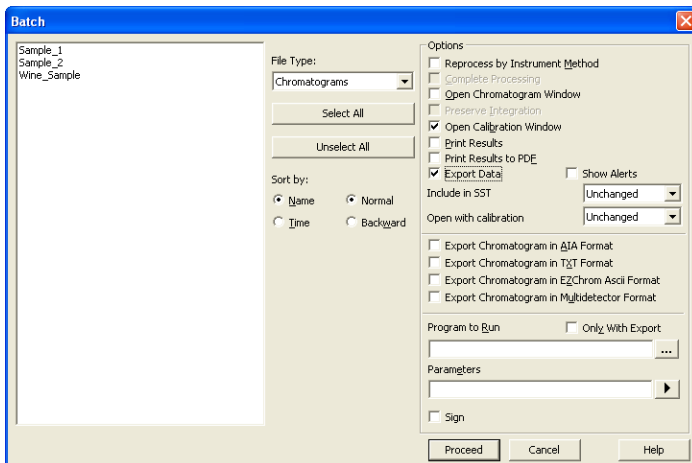


Fig 10: Batch dialog

The *Run Program* option in the **PostRun Setting** can be used to start some application such as MS Excel macro using the exported file name as parameter (variable %e). This could be used to automatically invoke the import of exported data to the **LIMS**

## 4 Review measured chromatograms

To review a series of chromatograms, the *Open Chromatogram Sequentially* command in the **Chromatogram** window is useful.

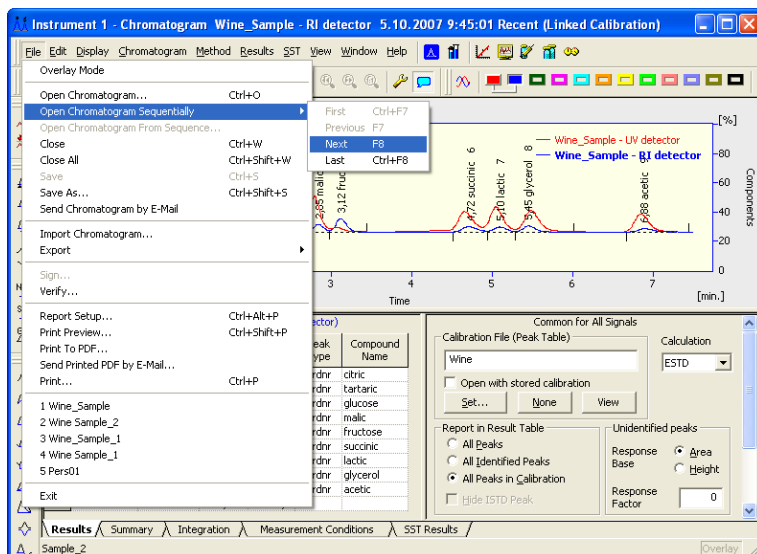


Fig 11: *Open Chromatogram Sequentially* menu in the **Chromatogram** window

You will use the wildcards (\*, ?) in the file open dialog to filter out the desired files and open one of them.

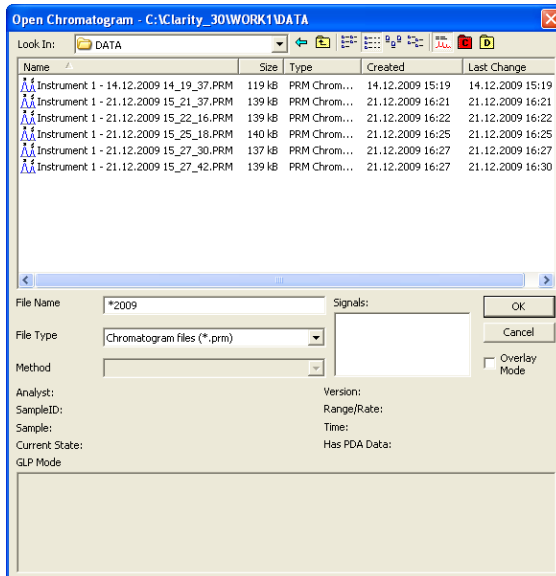


Fig 12: Open chromatogram with filter

For this reason, it is strongly recommended to use the *%variables* to create filenames automatically and to include all the info which could be used for searching/sorting the files.